

Result No.	Score	Query Match	Length	DB	ID	Description
1	824	26.1	164	4	US-09-621-976-5565	Sequence 5565, Ap
2	816	25.9	301	4	US-09-902-540-11184	Sequence 11184, A
3	783	24.8	336	4	US-09-270-767-44314	Sequence 44314, A
4	691.5	21.9	390	4	US-09-252-991A-26058	Sequence 26058, A
5	686	21.1	389	4	US-09-328-352-6380	Sequence 6380, Ap
6	650	20.6	384	4	US-09-648-004-6	Sequence 6, Appl
7	650	20.6	384	4	US-10-272-419-6	Sequence 6, Appl
8	623	19.6	387	4	US-09-328-352-6442	Sequence 6442, Ap
9	618.5	19.6	403	4	US-09-252-991A-27960	Sequence 27960, A
10	608	19.3	382	4	US-09-328-352-4850	Sequence 4850, Ap
11	604	19.2	432	4	US-09-949-016-6098	Sequence 6098, Ap
12	603.5	19.1	419	4	US-09-252-991A-31097	Sequence 31097, A
13	596	18.9	394	4	US-09-328-352-68001	Sequence 6801, Ap
14	595.5	18.9	409	3	US-09-364-230-30	Sequence 30, Appl
15	588.5	18.7	427	3	US-09-364-230-32	Sequence 32, Appl
16	588.5	18.7	459	4	US-09-949-016-10443	Sequence 10443, A
17	559.5	17.7	383	4	US-09-328-352-7081	Sequence 7081, Ap
18	546.5	17.3	421	4	US-09-949-016-5872	Sequence 5872, Ap
19	546.5	17.3	610	4	US-09-949-016-7708	Sequence 7708, Ap
20	538.5	17.1	331	4	US-09-902-540-15531	Sequence 15531, A
21	514.5	16.3	402	4	US-09-328-352-4281	Sequence 4281, Ap
22	501	15.9	424	4	US-09-252-991A-24653	Sequence 24653, A
23	495	15.7	399	4	US-09-328-352-4360	Sequence 4360, Ap
24	495	15.7	464	4	US-09-252-991A-33108	Sequence 33108, A
25	479	15.2	415	4	US-09-806-536A-13	Sequence 13, Appl
26	479	15.2	444	4	US-09-949-016-10163	Sequence 10163, A
27	472	15.0	282	4	US-09-252-991A-29144	Sequence 29144, A

```
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11184
LENGTH: 601
TYPE: PRT
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(601)
OTHER INFORMATION: unsure at all xaa locations
US-09-902-540-11184

Query Match      25.9%; Score 816; DB 4; Length 601;
Best Local Similarity 36.1%; Pred. No. 7.9e-74;
Matches 214; Conservative 92; Mismatches 197; Indels 90; Gaps 16;

QY 54 FPPPEVSDQL-----NEINQFLGVEKFFTEV--DSRKID-OEGKIPDETLEKLS 103
Db 19 FLPEEVGSARILPTETBEORLFFKFTALQFSREQVPLSERIEAKDNALLRQLRQAGE 78
QY 104 LGLFGLQVPEYCGLGFSNTMYSLRGLIISMDGSIITVTLAAHQAGLKGIIILAGTEEOKA 163
Db 79 LGLLSVDIPAYGGTGLDKTTSLLLAELSNGSWSTFGAHTGIGTLPVIFWFGNAEQKA 138
-QY 164 KYLPKLAGSHIAAFCLITEPASGSDAASIRATLSSEDKKHYYILNGSKWMTNGGLANIF 223
Db 139 KYLPKLAGTGBWAAYALTEQSGSDALGAKTAVLSPDGKHWILNGSKLYITNAADFV 198
QY 224 TVFAKTEVDSGSKDKITAFIVERDPFGVTGKPEDKLGIRGNTCEVHFENTKIPVE 293
Db 199 VVFAKV-----DG---DKFTGFIVEKDTPLGTVGPEEHKMGIRGSSSTCPLYFEDARVPVE 250
QY 284 NILGEVGDGFKVAMNINLSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFLQ 343
Db 251 NQGEVGGKHIAFNIINLYGRLLKLGACVGMKLOQNALRFTQERKQFNAPIVQPLSR 310
QY 344 EKFPALMAQKAYVMESMTYLTAGML-----DQGF-----PDCEIAAMVKVFS 386
Db 311 EKLARMAALVAVESMTYRTAGLVADRLGQGDADPYEARLLLEAVEEYAEISSIMKVHG 370
QY 387 SEAAQCVSEALQILGLGTRDYPYRIIRDTRILLIFEGTNEILRMVIALTGLQHAGR 446
Db 371 SESFGLVDDAVQLHGGAGYIEYPVRSYRDARINKIFEGTNEINRMLITGMMLKRAVR 430
QY 447 ILTTRIHELQO-AKVSTVMDTVGR-----RLRDSLGRITVDLGLTGNHGVVHPSLADSAN 499
Db 431 -----GDLPLFAMAGNVAELSRGERPRARVQDALAPQVAAEAAGKHALH-----476
QY 500 KFEENTYCFGRV--ETLLLRFGKTIMEBQVLKRVANILINLYGMTAVLSRASRS-----553
Db 477 -----GLRVAET-----FGPELHQEVLAAALSDVMDAPALDSMVTTRQATSG 523
QY 554 -----IRIGL-----RNHDE-EVLLANTFCVEAYLONLFLSLDLDKXAP 591
Db 524 ALDPRVAMTQLYALDAIPRAYDTRRALCATLKGALDQELERGLTLDVFTTP 576

RESULT 3
US-09-270-767-44314
; Sequence 44314, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
```

```
SEQ ID NO 44314
LENGTH: 336
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-44314

Query Match      24.8%; Score 783; DB 4; Length 336;
Best Local Similarity 49.3%; Pred. No. 6.7e-71;
Matches 169; Conservative 54; Mismatches 104; Indels 16; Gaps 5;

QY 218 GLANITVFAKTEVD--SDGSVKDKITAFIVERDGGTNGKPKDKLGRGNTCEVHEE 276
Db 3 GIAEIMTVFAQTEQVDPKTGKKDKVTAIFIVERSFGVTNGPPEKKMGKASNTAEVFE 62
QY 277 NTKIPVENILGEVGDGFKVAMNINLSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRL 336
Db 63 DVKIPENVLGEGGDFKVMNINLNGRFGMGATISGTMKKICIEQATEHANNRVQGGKL 122
QY 337 SBFGLIQEKFALMAQKAYVMESMTYLTAGMLDQPGFPDCEIAAMVKVFSSEAAQCVSE 396
Db 123 KNYGSIQEKLAQMNILQYATESMAFTISQNMW-AGSKDYHLEAAISKIYASESAWVVCDE 181
QY 397 ALQIIGLGYTRDYPYRIIRDTRILLIFEGTNEILRMVIALTGLQHAGRILTRIHCLK 456
Db 182 AIQILGGMGYMDTGLERVLRLRIFRIPEGTNDILRLFIALTGIQYAG-----SHLKEIQ 237
QY 457 Q-----AKVSTVMDTVGRRLRDSLGRITVDLGLTGNHGVVHPSLADSANKFBENTYCFGR 510
Db 238 RAFKPSANLGLIFKEASR-----AASVGLGTDLSGHVVGELLPYAKKTAHCIDLFQ 293
QY 511 TVETLLRFGKTIMEBQVLKRVANILINLYGMTAVLSRASRS 553
Db 294 SVEELLRYKNIVNEQILLRLANAAIDYAMVWVVTQSRSSRA 336

RESULT 4
US-09-252-991A-26058
; Sequence 26058, Application US/09252991A
; Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26058
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26058

Query Match      21.9%; Score 691.5; DB 4; Length 390;
Best Local Similarity 37.8%; Pred. No. 1.8e-61;
Matches 147; Conservative 82; Mismatches 121; Indels 39; Gaps 8;

QY 67 INQFLGVEKFFTEV--DSRKIDQEGKIPDETLEKLSLGLFGLQVPEYGGIGLPSNTM 124
Db 14 LNLLEDLSIRQVRESLVPHEQVAETDRIPEAIARMREMGFLGLSIPAYGGIG-----68
QY 125 YSLRGEIISMDGSIITV-----LAAHQALGLKGIILAGTEEOKAKYLPKLAS 171
Db 69 -----VTMEEEVSTAFELGRTPSPRSLGTNGNGISQGIIVIDGTEERKRYLPRLAS 121
QY 172 GEHIAAFCLTEPASGSDAASIRATLSSEDKKHYYILNGSKWMTNGGLANIFTVFAKTEV 231
Db 122 GELLSSFCLETPDSDAASLKTTAV--RDGEHYVLNGTKRFTINAPQAGIYTVWART--177
```

```
QY 232 VSDGSKDK--ITAFIVERDFGVNCKPEDKLGIRGNTCEVHPENTKIPVENILGEV 289
Db 178 ---DPAIRAGGSAFVERGTGLSLGKPDRCMGKGARTCDVIFDCCRPASQLIGV 234
QY 290 -GDGFKVAMNLSRFGSMGVVAGLLKRLIEMTAETACRQKFNKRLSEFGLIOEKFAL 348
Db 235 EGVGFTAMKVLKGRHLHIAVCVGAERMLEDALYALERKQFGQPIAEFQIQLAMLAD 294
QY 349 MAQKAYMESMTYLTAGMLDPQFPDSCIEAAMVVPSSAAWQCVSEALQILGLGYTR 408
Db 295 SKAEAYAARCMWIDAARQDEG--RDVGTASCAKLPASEMCGRVADRAVQIFGGAGYIG 352
QY 409 DYPYERILDRILLIFEGTNEILRMVIA 437
Db 353 DYGIERYDRVRLFRYIEGTTQIQLLIA 381

RESULT 5
US-09-328-352-6380
; Sequence 6380, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: GAY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6380
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6380

Query Match 21.1%; Score 666; DB 4; Length 389;
Best Local Similarity 38.8%; Pred. No. 7.3e-59;
Matches 150; Conservative 79; Mismatches 148; Indels 16; Gaps 8;

QY 58 EVSQDELNEINQFLGPVEKFFTEVDNR--KIDQEGKIPDETLEKLSLGLQVPEEY 115
Db 5 QMRDE-GMLEQLLSITRDFVKNELIPRENEVEKXIPDDIVQQWRELGLFLTIPEEY 63

QY 116 GGLGFNTMYSLG-ELIISMDGSITVTLAAHQAIKGLIAGTEBQKAKYLPKLASGEH 174
Db 64 GGLGITMEBEVRVAFELGQTSAPFRSLIGTNGIGSSAILIDGTBEQOKYLPYASGEI 123

QY 175 IAAFCLETPASGSDAASIRSRATLSEDKKHYILNGSKVITNGGLANIETVFAKT--EVV 232
Db 124 IGSFCLTEPESGSDAASLTSV--KDGDFYVLNGTKRFTTNAPHAAETFTWARTNPEIK 181

QY 233 DSDGSKDKITAFIVERDFGVNCKPEDKLGIRGNTCEVHPENTKIPVENILGEV-GD 291
Db 182 GSGG-----ISAFLEANTPGITLGIKIDQWKGQSGHTCDVIFENCVRVASALIGVEGV 236

QY 292 GFKVAMNLSRFGSMGVVAGLLKRLIEMTAETACRQKFNKRLSEFGLIOEKFALMAQ 351
Db 237 GFKTAMKVLKGRHLHIGAYSVGVAERMLNDALNYAIERKQFGQPIANFQIQLAMLADSKA 296

QY 352 KAYMESMTYLTAGMLDPQFPDSCIEAAMVVPSSAAWQCVSEALQILGLGYTRDYP 411
Db 297 EYIAAKCMWLDAARRDNG--ENISTEASCAKMFATEMCGRVADRCVQIHGGAGYISEYA 354

QY 412 YERILDRILLIFEGTNEILRMVIALTGLQHA 444
Db 355 IERYDRVRLFRYIEGTTQVQQLIIANNMIREA 387;

RESULT 6
US-09-648-004-6
; Sequence 6, Application US/09648004
; Patent No. 6496242
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL-1341-A
; CURRENT APPLICATION NUMBER: US/09/648,004
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-648-004-6

Query Match 20.8%; Score 650; DB 4; Length 384;
Best Local Similarity 38.6%; Pred. No. 3.1e-57;
Matches 154; Conservative 77; Mismatches 132; Indels 36; Gaps 11;

QY 61 QDELNE---INQFLGPVEKFFTEVDNRKIDQEGKIPDETLEKLSLGLQVPEEY 116
Db 5 QDTLNLQVDMIROFDGV-LIPNEEI-----VAETDEIPAEIVQOMKELGFLTIPEEY 59

QY 117 GLGFNTMYSLR---GEIISMDGSITVTLAAHQAIKGLIAGTEBQKAKYLPKLASGE 173
Db 60 GLGL--TWEEVYIAFELGRTSPAFRSLICTNNGIGSSGLIIDGSEQKQYFLPRLASGE 117

QY 174 HIAFCLTEPAGSDAASIRSRATLSEDKKHYILNGSKVITNGGLANIETVFAK--TEV 231
Db 118 IIGSFCLTEPDSGSDAASLKTAV--KDGPHYILNGTKRYITNAPHAGVFTWARTSTEI 175

QY 232 VSDGSKDKITAFIVERDFGVNCKPEDKLGIRGNTCEVHPENTKIPVENILGEV-G 290
Db 176 KGTGG-----ISAFIVDSKTPGISLGRKDKMGQKGAHTCDVIFENCVRVASALIGVEG 230

QY 291 DGFKVAMNLSRFGSMGVVAGLLKRLIEMTAETACRQKFNKRLSEFGLIQ-----EK 345
Db 231 VGFKTAMKVLKGRHLHIAALSVAATRMLEDSLOYAVERKQFGQATANFQIQLAMLADSK 290

QY 346 FALMAQKAYMESMTYLTAGMLDPQFPDSCIEAAMVVPSSAAWQCVSEALQILGLGL 405
Db 291 AEIYAAKCMWLDAARLDAGQ-----NVSTEASCAKMFATEMCGRVADRCVQIHGGAG 343

QY 406 YTRDYPYERILDRILLIFEGTNEILRMVIALTGLQHA 444
Db 344 YISEYAIERYDRVRLFRYIEGTTQIQQVIIARNMIREA 382

RESULT 7
US-10-272-419-6
; Sequence 6, Application US/10272419
; Patent No. 6794165
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: CL1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419
; CURRENT FILING DATE: 2002-10-16
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-6
```

Query Match 20.6%; Score 650; DB 4; Length 384;
Best Local Similarity 38.6%; Pred. No. 3.1e-57;
Matches 154; Conservative 77; Mismatches 132; Indels 36; Gaps 11;
QY 61 QDELNE----INQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYG 116
DB 5 QDTLNQLVDMIRQFVQGV-LIPNEEI---VAETDEIPAEIVQOMKELGFLGFTIPEEYE 59
QY 117 GLGFSNTWYRL---GHIISMDGSIWTLAAHQAGLKGIIILAGTEQKAKYLPKLASGE 173
DB 60 GLGL--TMEBEVIAFELGRTSPAFRSLIGTNNIGSSGLIIDGSEEQKQYFLPLASGE 117
QY 174 HIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPTVFAK--TEV 231
DB 118 IISGFCUTEPSDSDAASLKTAV--KGDHYILNGTKRYITNAPHAGVFTWARTSTEI 175
QY 232 VDSGSKDKITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENILGEV-G 290
DB 176 KGTGG-----ISAFIVDSKTPGISLGRKDKMKQKGAHTCDVIFENCRI PASALIGVEG 230
QY 291 DGFVAMNINSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIQ-----EK 345
DB 231 VGFKTAMKVLDKRIHIAALSVAATRMLEDLSQYAVERKQFGQAIANFOLIQMLADSK 290
QY 346 FALMAOKAYVYEMSTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLG 405
DB 291 AEIYAAKCVLDARLDAQ-----NVSTASCAKMFATEMCGRVADRGVQIHHGGAG 343
QY 406 YTRDYPYERILDRILLIPEGTNEILRMVIALTLQHA 444
DB 344 YISEYAIERYDVRFLRYEGTQIQOQVIAARNMIREA 382

RESULT 8

US-09-328-352-6442
; Sequence 6442, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-03-PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6442
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6442

Query Match 19.8%; Score 623; DB 4; Length 387;
Best Local Similarity 36.8%; Pred. No. 1.8e-54;
Matches 145; Conservative 79; Mismatches 130; Indels 40; Gaps 10;
QY 61 QDELNEINQFLGPEKFFTEEV---DSRKIDQEGKIPDETLEKLSGLGFLGQVPEEYG 117
DB 9 QETLNQLVDMI-----RQFVECVLI PHENEVAETDEIPDIVEQMKALGFLGFTIPEEYG 64
QY 118 LGSNTWYRLGHIISMDGSIWTLAAHQAGLKGIIILAGTEQKAK 164
DB 65 LG-----LTMEBEVYVAFELGRTSPAFRSLIGTNNIGSSGLIIDGTEAQKSF 112
QY 165 YLPKLASGEHIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPT 224
DB 113 FLPLARGEVISSFCLTEPDAGSDAASLKTAV--KGDFFYVLNGTKRFTNAPHAGVFT 170
QY 225 VFAKTEVDSGSKDKITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVEN 284
DB 171 VMARTN-FDIKGA--SGISAFIVDSQTPGISLGRKDKMKQKGVHTCDVIFENCRI PASA 227
QY 285 ILGEV-GDGFVKVAMNINSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIQ 343

DB 228 LTGGVEGVGFKTAMKVLDRHIAALSVAATRMDDSLNIAIRKQFGQPIAEFQLIQ 287
QY 344 EKFAALMAOKAYVYEMSTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAWQCVSEALQILGG 403
DB 288 AMLADSKAEIYAAKCV-LDAARLRDAG-QNVSTASCAKMFATEMCGRVADRCVQIHGG 345
QY 404 LGYTRDYPYERILDRILLIPEGTNEILRMVIA 437
DB 346 AGYISEYAIERYDVRFLRYEGTQIQOQVIAA 379

RESULT 9

US-09-252-991A-27960
; Sequence 27960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27960
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27960

Query Match 19.6%; Score 618.5; DB 4; Length 403;
Best Local Similarity 37.5%; Pred. No. 5.4e-54;
Matches 149; Conservative 71; Mismatches 148; Indels 29; Gaps 8;

QY 52 EYVFPFVSQDELNEINQFLGPEKFFTEEVDSR--KIDQEGKIPDETLEKLSGLGFLG 109
DB 15 ESMYFSLNFALGETIDMLRDQVRGFAELQPRAAQIDQDNQFPMDMWRKFGEMGLLGI 74
QY 110 QYPEEYGGFLGFSNTWYRLGELIIS--MDGSITVTLAAHQAGLKGIIILAGTEQKAKYLPK 168
DB 75 TVDEEYGSALCYLAHAVVMEISASASVALSYGAHNLVCVQIKRNGNAEQKARYLPA 134
QY 169 LASGEHIAAFCLTEPASGSDAASIRSRATLSDEKHYILNGSKWITNGGLANIPTVFAK 228
DB 135 LVSGEHIGALAMSEPNAGSDVVMKLRADRVGDR--FVLNGSKWITNGPDATHTVIVAK 192
QY 229 TEVDSGSKDKK---ITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVEN 284
DB 193 TDA-----DKGAHGITAFIVERDWDGKFSRGPCKLKLGMGRGNTCELI FQDVEVPEEN 244
QY 285 ILGEVGDGFKVAMNINSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOE 344
DB 245 VLGVANGGVKVLMSGLDYERVVLSGPGVIMQACNDVVVPYIHDRQFGQSIGEFQLVQ 304
QY 345 KF-----ALMAQKAYVYEMSTYLTAGMLDQPGFPDCSIEAAMVKVFSSEAAWQCVSEALQ 399
DB 305 KVADMYTALNASRAYL-----YAVAAACDRG--ETTRKDAAGVILYSAERATQMALDAIQ 357
QY 400 ILGGIYTRDYPYERILDRILLIPEGTNEILRMVYI 436
DB 358 ILGGYINIEFTGRLRLDRAKLYEIGAGTSEIRMLI 394

RESULT 10

US-09-328-352-4850
; Sequence 4850, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4850
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4850

Query Match 19.3%; Score 608; DB 4; Length 382;
Best Local Similarity 37.5%; Pred. No. 5.8e-53;
Matches 142; Conservative 71; Mismatches 154; Indels 12; Gaps 6;
QY 63 ELNEINQFLGPGVEKFFTEE---VDSRKIDQEGKIPDETLEKLSGLGLFGLQVPEEYGGGLG 119
DB 9 QTEEQILLRDMAKSFAQIKPNASDWDGDTGTFKPTLTOMQGLGFMGLMSEEWGGSD 68
QY 120 FSNMTY-SRGEIISMDGSIITVTLAAHQAIGLKGIIILAGTEQKAKYLPKLASGEHIAAF 178
DB 69 TGNLAYVLAEEVAADGATSTTMSVHNSVGCVPILKPGTDEQKERFLKPLAQGEMIGAF 128
QY 179 CLTEPASGDAASIRSATLSEDKHYILNGSKVWITNGGLANIFTVPFAKTEVWDSGV 238
DB 129 ALTEPTGSDAAAIKTRAV---KQDDYIILNGAKQFITSNGNAGVITVFAVTD-----PSAG 182
QY 239 KDKITAFIVERDFGGVTKGPKEDKLGIRGNTCEVHFENTKIPVENILGEVGGPKVAMN 298
DB 183 KGISAFILVPTGPGVEIRVEEKLGHASDTQIALTVRIHKSMLMGKEGGLKIALA 242
QY 299 ILSGRFSMGVSVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOBKALMAQKAYVMS 358
DB 243 NLEGGRIAGAAQAVGLARAALAEATYAKERITTFGKPIFEHQTIAPRLASMAIEAARQ 302
QY 359 MYLITAGMLDQGFPPDCSIEAMVKVFSSEAAWQCSEALQILGGLGYTRDYPYERILRD 418
DB 303 LVHY-AARLKEAGQP-CLNEASMAKLFASEMTERVCSALQVFGGYGLRDPPIERYRD 360
QY 419 TRILLIFEGTNEILRMVIA 437
DB 361 ARICQIYEGTSDIQLRVIA 379

RESULT 11
US-09-949-016-6098
; Sequence 6098, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6098
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6098

Query Match 19.2%; Score 604; DB 4; Length 432;
Best Local Similarity 35.9%; Pred. No. 1.8e-52;
Matches 157; Conservative 81; Mismatches 155; Indels 44; Gaps 14;

QY 19 GLVSTANRRLLRTSPVPAPAKELFLGKIKKKEVFP-PPEVSQDE--LINEINQ--FLGP 73
DB 3 GLAV-----RLLRGSRLLR-----RNFELTCLSSWKIPPHVSKSSQSEALLNITNGIHFAF 53
QY 74 VEKFFTEEVDSRK-----IDQEGKIPDETLEKLSGLGLFGLQVPEEYGG 117
DB 54 LOTFDEENMIKSSVKVFAQEQIAPLVSTMDENSRMEKSVIQLFOQGLMGIEVDPEYGG 113
QY 118 LG--FSNTMYSRIGEIIISMDGSIITVTLAAHQAIGLKGIIILAGTEQKAKYLPKLASGEHI 175
DB 114 TGASFLSLTVLV-IEELAKVDASVAVFCEIQNTLINTLRKHGTEQKATYLPQLTT-EKV 171
QY 176 AAFCLTEPASGDAASIRSATLSEDKHYILNGSKVWITNGGLANIFTVPFAKTEVWDS 235
DB 172 GSFCLEAGAGSDSFALKTRADKEG--YYVLNGSRWISSAEHAGFLVMANV-----D 224
QY 236 GSVKDK-ITAFIVERDFGGVTKGPKEDKLGIRGNTCEVHFENTKIPVENILGEVGGPK 294
DB 225 PTIGYKGIITSLFVDRDTPGLHIGKPKENKLGLRASSTCPLTFENVKVPANILGQIGHYK 284
QY 295 VAMNIIINSGRFSMGVSVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOBKALMAQKAY 354
DB 285 YAGISLNEGRIGIAAQMGLAQCQPDYTIPIYKERIQFGKRLDFDFOGLQHOVAHVATQLE 344
QY 355 VMESMTYLTAGMLDQGFPPDCSIEAMVKVFSSEAAWQCSEALQILGGLGYTRDYPYER 414
DB 345 AARLLTYNAARLL-EAGKPFIK-EASMAKYAYASEIAGOTTSCIEWMGWGVYTKDPVEK 402
QY 415 ILRDTFRILLIFEGTNEI 431
DB 403 YFRDAKIGTIYEGASNI 419

RESULT 12
US-09-252-991A-31097
; Sequence 31097, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31097
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31097

Query Match 19.1%; Score 603.5; DB 4; Length 419;
Best Local Similarity 38.7%; Pred. No. 2e-52;
Matches 136; Conservative 67; Mismatches 139; Indels 9; Gaps 6;
QY 88 DOEGKIPDETLEKLSGLGLFGLQVPEEYGGGLGFSNTMYS-RLGEIISMDGSIITVLAHQ 146
DB 74 DREHRFPAAIREMADLGLGLMLVPEEWGGAQTGHAYAMALEEETAAAGGACSTMSVHN 133
QY 147 AIGLKGIIILAGTEQKAKYLPKLASGEHIAAACLTEPASGDAASIRSATLSEDKHYI 206
DB 134 SVGCMPIHKFGSAEQKERFLRPLAQGSLGVALTEPQAGSDASFUKTRA--RRDGDHYV 191
QY 207 LNSGKVWITNGGLANIFTVPFAKTEVWDSGVSKDKITAFIVERDFGGVTKGPKEDKLGIR 266
DB 192 LNKAKQFITSQSHAGNVIFA---VTDPDAG-KRGISAFIVPTDTPGYEVVRIEDKLGQH 247
QY 267 GSNTCEVHFENTKIPVENILGEVGGPKVAMNIIINSGRFSMGVSVAGLLKRLIEMTAEYA 326


```
Qy 69 QPLGPVEKPFTEV--DSRKIDQEGKIPDTELEKLSLG---LFLQVPEEYGGGLGFSNT 123
Db 55 QFKESVAQFATENIAPHASKIDQNTNYPKE-VNLWKSMEFNLLGITAPEEYGGGLGGLYL 113
Qy 124 MYS-RLGEIISMDGSITVTLLAAHQAIGLGIILAGTEEOKAKYLPKLAGGEHIAAFCLTE 182
Db 114 YHCIAEEISRASGSVGLSGAHSNLCINOLVRNGSPAQKEKYLPLKISGDHVGALAMSE 173
Qy 183 PASGSDAASIRSRATLSEDKKHVILNGSKWITNGGLANIFTVFAKTEV-VDSGDSVKDK 241
Db 174 PNSGSDVWSMKCKADRVG--GYVLNGNKMWCTNGPVAQTLVVYAKTDITAGSKG----- 226
Qy 242 ITAFIVERDFGGVTNGKPEDKLGIRGNTCEVHFENTKIPVENILGEVGDGPKVANNILN 301
Db 227 ITAFIIEKMGPGNTAQKLDKLGMRGSDTCELVFENCVPDENILGKGGKGVYVWMSGLD 286
Qy 302 SGRFSMGSVVAGLKLKLIEMTAEYACTRKQFNKRLSEFGLIOEKEFA-----LMAOKAYVM 356
Db 287 LERLVLAAGPLGIMQACLDVLPYVRQEQFGPIGEFQIQGIADMYTSLQSSRSYVY 346
Qy 357 ESMYTLTAGMLDQFPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERIL 416
Db 347 SVARDCDNGKVP---KDC---AGAILCAAERATQVALQIQICLGNGGVVNEYPTGRLL 399
Qy 417 RDRILLIFEGTNEILRMVI 436
Db 400 RDAKLYEIGAGTSEIRRMII 419
```

Search completed: April 25, 2005, 17:28:03
Job time : 45 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 17:24:59 ; Search time 134 Seconds
(without alignments)
1542.263 Million cell updates/sec

Title: US-09-945-326-2
Perfect score: 3153
Sequence: 1 MSGCGLFRTTAAARACRGL.....SQIILEKRAYICAHPLDRTC 621

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US10D_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3153	100.0	621	9 US-09-945-326-2	Sequence 2, Appli
2	3153	100.0	621	14 US-10-168-274-24	Sequence 24, Appl
3	3153	100.0	621	15 US-10-112-944-420	Sequence 420, App
4	3153	100.0	621	16 US-10-408-765A-1059	Sequence 1059, Ap
5	3153	100.0	621	16 US-10-408-765A-2053	Sequence 2053, Ap
6	3129	99.2	628	15 US-10-112-944-869	Sequence 869, App
7	1360	43.1	655	15 US-10-362-537-10	Sequence 10, Appl
8	1356.5	43.0	653	15 US-10-362-537-9	Sequence 9, Appli
9	1345	42.7	655	15 US-10-362-537-11	Sequence 11, Appl
10	1308	41.5	655	15 US-10-362-537-1	Sequence 1, Appli
11	1308	41.5	655	16 US-10-408-765A-534	Sequence 534, App
12	1299	41.2	655	16 US-10-408-765A-320	Sequence 320, App
13	1210.5	38.4	613	15 US-10-369-493-5444	Sequence 5444, Ap

14	954	30.3	188	16	US-10-408-765A-1442	Sequence 1442, Ap
15	954	30.3	188	16	US-10-408-765A-2052	Sequence 2052, Ap
16	844.5	26.8	594	15	US-10-369-493-16704	Sequence 16704, A
17	821	26.0	594	15	US-10-369-493-17429	Sequence 17429, A
18	816	25.9	581	15	US-10-369-493-19424	Sequence 19424, A
19	815.5	25.9	594	15	US-10-369-493-23285	Sequence 23285, A
20	798	25.3	585	15	US-10-369-493-9771	Sequence 9771, Ap
21	795.5	25.2	583	15	US-10-369-493-10383	Sequence 10383, A
22	765	24.3	583	15	US-10-369-493-16614	Sequence 16614, A
23	704	22.3	373	15	US-10-369-493-16614	Sequence 16614, A
24	699	22.2	382	15	US-10-369-493-16795	Sequence 16795, A
25	690	21.9	379	15	US-10-369-493-17460	Sequence 17460, A
26	686.5	21.8	377	15	US-10-369-493-9826	Sequence 9826, Ap
27	682	21.6	378	15	US-10-369-493-23196	Sequence 23196, A
28	678	21.5	381	15	US-10-369-493-16918	Sequence 16918, A
29	675.5	21.4	379	15	US-10-369-493-16613	Sequence 16613, A
30	659.5	20.9	646	14	US-10-156-761-10104	Sequence 10104, A
31	658	20.9	380	15	US-10-369-493-17459	Sequence 17459, A
32	652.5	20.7	379	15	US-10-369-493-23337	Sequence 23337, A
33	652	20.7	387	15	US-10-369-493-577	Sequence 577, App
34	650	20.6	384	14	US-10-272-419-6	Sequence 6, Appli
35	644.5	20.4	370	15	US-10-369-493-14087	Sequence 14087, A
36	641	20.3	375	15	US-10-369-493-8807	Sequence 8807, Ap
37	640	20.3	378	15	US-10-369-493-16449	Sequence 16449, A
38	633	20.1	375	15	US-10-369-493-17779	Sequence 17779, A
39	630.5	20.0	387	15	US-10-369-493-13698	Sequence 13698, A
40	629.5	20.0	381	15	US-10-369-493-546	Sequence 546, App
41	629	19.9	374	15	US-10-369-493-9830	Sequence 9830, Ap
42	626	19.9	373	15	US-10-369-493-11638	Sequence 11638, A
43	626	19.9	377	15	US-10-369-493-14685	Sequence 14685, A
44	625.5	19.8	379	15	US-10-369-493-10412	Sequence 10412, A
45	624	19.8	378	15	US-10-369-493-9086	Sequence 9086, Ap

ALIGNMENTS

RESULT 1

US-09-945-326-2
; Sequence 2, Application US/09945326
; Patent No. US20020127680A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Hunter, John Joseph
; TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MNI-187
; CURRENT APPLICATION NUMBER: US/09/945,326
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,831
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-326-2

Query Match 100.0%; Score 3153; DB 9; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.7e-270;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGCGLFRTTAAARACRGLVSTANRRLLRTSPVRAFAGKFLGKIKKVEFPPEVS 60
DB 1 MSGCGLFRTTAAARACRGLVSTANRRLLRTSPVRAFAGKFLGKIKKVEFPPEVS 60
QY 61 QDELNEINFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLGF 120
DB 61 QDELNEINFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLGF 120
QY 121 SNTMYSLRGEIISMGSGITVTTLAAHQAIKGLIGLITAGTEQAKYLPKLAGSHIIAFLC 180

Db 121 SNTWYRLGEEIISMDGSIITVTLAAHQAIIGLGIILAGTEBQAKYLPKLASGEHIAAFCL 180
Qy 181 TEPASGDAASIRSRATLSEDKKHYILNGSKWITNGGLANIETVFAKTEVDSDGSKVD 240
Db 181 TEPASGDAASIRSRATLSEDKKHYILNGSKWITNGGLANIETVFAKTEVDSDGSKVD 240
Qy 241 KITAFIVERDFGVTNGKPEDKLIRGNSNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
Db 241 KITAFIVERDFGVTNGKPEDKLIRGNSNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
Qy 301 NSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Db 301 NSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Qy 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
Db 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
Qy 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDTR 480
Db 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDTR 480
Qy 481 LGTGNHGVVHPHSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Db 481 LGTGNHGVVHPHSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Qy 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Db 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Qy 601 VSQQLKEKRAYICAHPLDRTC 621
Db 601 VSQQLKEKRAYICAHPLDRTC 621

RESULT 2

US-10-168-274-24
; Sequence 24, Application US/10168274
; Publication No. US20030124106A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: HILLMAN, Jennifer
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.
; TITLE OF INVENTION: HUMAN OXIDOREDUCTASE PROTEINS
; FILE REFERENCE: PF-0754 PCT
; CURRENT APPLICATION NUMBER: US/10/168,274
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/172,367
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124106A1 5540437CD1
US-10-168-274-24

Query Match 100.0%; Score 3153; DB 14; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.7e-270;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSGCGFLRTTAARACRGVLVSTANRLRTSPVRAFAKELFLGKIKKKEVFPPEVPS 60
Db 1 MSGCGFLRTTAARACRGVLVSTANRLRTSPVRAFAKELFLGKIKKKEVFPPEVPS 60

Qy 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGLQVPEEYGLGF 120
Db 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGLQVPEEYGLGF 120
Qy 121 SNTWYRLGEEIISMDGSIITVTLAAHQAIIGLGIILAGTEBQAKYLPKLASGEHIAAFCL 180
Db 121 SNTWYRLGEEIISMDGSIITVTLAAHQAIIGLGIILAGTEBQAKYLPKLASGEHIAAFCL 180
Qy 181 TEPASGDAASIRSRATLSEDKKHYILNGSKWITNGGLANIETVFAKTEVDSDGSKVD 240
Db 181 TEPASGDAASIRSRATLSEDKKHYILNGSKWITNGGLANIETVFAKTEVDSDGSKVD 240
Qy 241 KITAFIVERDFGVTNGKPEDKLIRGNSNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
Db 241 KITAFIVERDFGVTNGKPEDKLIRGNSNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
Qy 301 NSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Db 301 NSGRFSMGSVVAGLLKRLIEMTAETACTRKQFNKRLSEFGLIOEKPALMAQKAYVMESMT 360
Qy 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
Db 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTR 420
Qy 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDTR 480
Db 421 ILLIFEGTNEILRMVYIALTGLQHAGRLITRIHELKQAKVSTVMDTVGRRRLDSLGRDTR 480
Qy 481 LGTGNHGVVHPHSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Db 481 LGTGNHGVVHPHSLADSANKFEENTYCFGRVTETLLRFKGTIMESQVLKRVANILINL 540
Qy 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Db 541 YGMTAVLSRASRSIRIGLRNHDHVEVLANTFCVEAYLQNLFSLSQDKYAPENLDQIKK 600
Qy 601 VSQQLKEKRAYICAHPLDRTC 621
Db 601 VSQQLKEKRAYICAHPLDRTC 621

RESULT 3

US-10-112-944-420
; Sequence 420, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: US 09/552,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/577,408
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 924
 ; SOFTWARE: pt_genes version 5.0
 ; SEQ ID NO 420
 ; LENGTH: 621
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-112-944-420

Query Match 100.0%; Score 3153; DB 15; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2.7e-270;
 Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAKELFLGKIKKKEVFPPEVS 60
   |||||
DB 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAKELFLGKIKKKEVFPPEVS 60
   |||||

QY 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLQVPEYGGIGF 120
   |||||
DB 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLQVPEYGGIGF 120
   |||||

QY 121 SNTMYSLRGEIISMDGSIITVTLAAHQAIKGLIILAGTEQAKYLPKLASGEHIAAFCL 180
   |||||
DB 121 SNTMYSLRGEIISMDGSIITVTLAAHQAIKGLIILAGTEQAKYLPKLASGEHIAAFCL 180
   |||||

QY 181 TEPASGSDAASIRSRATLSEDKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
   |||||
DB 181 TEPASGSDAASIRSRATLSEDKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
   |||||

QY 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGPKVAMNII 300
   |||||
DB 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGPKVAMNII 300
   |||||

QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
   |||||
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
   |||||

QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDR 420
   |||||
DB 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDR 420
   |||||

QY 421 ILLIFEGTNEILRMVIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
   |||||
DB 421 ILLIFEGTNEILRMVIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
   |||||

QY 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
   |||||
DB 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
   |||||

QY 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
   |||||
DB 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
   |||||

QY 601 VSQIILEKRAYICAHPLDRTC 621
   |||||
DB 601 VSQIILEKRAYICAHPLDRTC 621
   |||||
  
```

RESULT 4

US-10-408-765A-1059
 ; Sequence 1059, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1059
 ; LENGTH: 621
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1059

Query Match 100.0%; Score 3153; DB 16; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2.7e-270;
 Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAKELFLGKIKKKEVFPPEVS 60
   |||||
DB 1 MSCGGLFLRTTAARACRGLVWSTANRLLRTSPVRAFAKELFLGKIKKKEVFPPEVS 60
   |||||

QY 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLQVPEYGGIGF 120
   |||||
DB 61 QDELNEINQFLGPEKFFTEEVDSRKIDQEGKIPDETLEKLSGLGFLQVPEYGGIGF 120
   |||||

QY 121 SNTMYSLRGEIISMDGSIITVTLAAHQAIKGLIILAGTEQAKYLPKLASGEHIAAFCL 180
   |||||
DB 121 SNTMYSLRGEIISMDGSIITVTLAAHQAIKGLIILAGTEQAKYLPKLASGEHIAAFCL 180
   |||||

QY 181 TEPASGSDAASIRSRATLSEDKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
   |||||
DB 181 TEPASGSDAASIRSRATLSEDKHYILNGSKWITNGGLANIPTVFAKTEVDSGSKVD 240
   |||||

QY 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGPKVAMNII 300
   |||||
DB 241 KITAFIVERDFGVTNGKPEDKLGIRGNTCEVHFENTKIPVENIILGEVGDGPKVAMNII 300
   |||||

QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
   |||||
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRQFNKRLSEFGLIOEKFPALMAQKAYVMESMT 360
   |||||

QY 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDR 420
   |||||
DB 361 YLTAGMLDQPGPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDR 420
   |||||

QY 421 ILLIFEGTNEILRMVIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
   |||||
DB 421 ILLIFEGTNEILRMVIALTGLQHAGRIILTRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
   |||||

QY 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
   |||||
DB 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTIMEQOLVKRVANILINL 540
   |||||

QY 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
   |||||
DB 541 YGMTAVLSRASRSIRIGLRNHDHEVLANTFCVEAYLQNLFSLSQLDKYPENLDEQIKK 600
   |||||

QY 601 VSQIILEKRAYICAHPLDRTC 621
   |||||
DB 601 VSQIILEKRAYICAHPLDRTC 621
   |||||
  
```

RESULT 5

US-10-408-765A-2053
 ; Sequence 2053, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2053
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2053

Query Match 100.0%; Score 3153; DB 16; Length 621;
Best Local Similarity 100.0%; Pred. No. 2.7e-270;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGCGFLRTTAAARACRGLVSTANRLRLTSPVPVAFKELFLGKIKKKEVFPPEVS 60
DB 1 MSGCGFLRTTAAARACRGLVSTANRLRLTSPVPVAFKELFLGKIKKKEVFPPEVS 60

QY 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120
DB 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120

QY 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEQKAKYLPKLASGEHIAAFCL 180
DB 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEQKAKYLPKLASGEHIAAFCL 180

QY 181 TEPASGDAASIRSRATLSDDKKHYILNGSKVITNGGLANITVFAKTEVVDSDGSVKD 240
DB 181 TEPASGDAASIRSRATLSDDKKHYILNGSKVITNGGLANITVFAKTEVVDSDGSVKD 240

QY 241 KITAFIVERDFGGVTKGPKDGLIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
DB 241 KITAFIVERDFGGVTKGPKDGLIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300

QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVWESMT 360
DB 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVWESMT 360

QY 361 YLTAGMLDQPGFPDPCSTEAAMVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDRTR 420
DB 361 YLTAGMLDQPGFPDPCSTEAAMVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDRTR 420

QY 421 ILIIFEGTNEILRMVIALTGLQHAGRIITRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480
DB 421 ILIIFEGTNEILRMVIALTGLQHAGRIITRIHELKQAKVSTVMDTVGRRLRDSLGRTVD 480

QY 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTTMESQLVKRVANILINL 540
DB 481 LGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLRFGKTTMESQLVKRVANILINL 540

QY 541 YGMTAVLSRASRSIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKVPENLDSQIKK 600
DB 541 YGMTAVLSRASRSIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKVPENLDSQIKK 600

QY 601 VSQOILEKRAYICAHPLDRTC 621
DB 601 VSQOILEKRAYICAHPLDRTC 621

RESULT 6

US-10-112-944-869
; Sequence 869, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi

; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 869
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(628)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fo
; OTHER INFORMATION: in Example 2
US-10-112-944-869

Query Match 99.2%; Score 3129; DB 15; Length 628;
Best Local Similarity 99.2%; Pred. No. 3.7e-268;
Matches 616; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSGCGFLRTTAAARACRGLVSTANRLRLTSPVPVAFKELFLGKIKKKEVFPPEVS 60
DB 8 MSGCGFLRTTAAARACRGLVSTANRLRLTSPVPVAFKELFLGKIKKKEVFPPEVS 67

QY 61 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 120
DB 68 QDELNEINQFLGPVEKFFTEEVDSRKIDQEGKIPDETLEKLSGLFGLQVPEYGGGLF 127

QY 121 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEQKAKYLPKLASGEHIAAFCL 180
DB 128 SNTWYRLGIIISMDGSIITVTLAAHQIAGLKIILAGTEQKAKYLPKLASGEHIAAFCL 187

QY 181 TEPASGDAASIRSRATLSDDKKHYILNGSKVITNGGLANITVFAKTEVVDSDGSVKD 240
DB 188 TEPASGDAASIRSRATLSDDKKHYILNGSKVITNGGLANITVFAKTEVVDSDGSVKD 247

QY 241 KITAFIVERDFGGVTKGPKDGLIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 300
DB 248 KITAFIVERDFGGVTKGPKDGLIRGNTCEVHFENTKIPVENILGEVGDGFKVAMNII 307

QY 301 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVWESMT 360
DB 308 NSGRFSGSVVAGLLKRLIEMTAETAYACTRKQFNKRLSEFGLIOEKFPALMAQKAYVWESMT 367

QY 361 YLTAGMLDQPGFPDPCSTEAAMVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDRTR 420
DB 361 YLTAGMLDQPGFPDPCSTEAAMVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDRTR 420

```
Db 368 YLTAGMLDQPGPPDCSIEAAWVKVFSSEAAWQCSEALQILGLGYTRDYPYERILDR 427
QY 421 ILLIFGTEILMYIALTGLQHAGRIITRIHELKQAKVSTYMDTVGRRRLRSLGRYVD 480
Db 428 ILLIFGTEILMYIALTGLQHAGRIITRIHELKQAKVSTYMDTVGRRRLRSLGRYVD 487
QY 481 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLIRFGKTTIMEQVLKRVANILINL 540
Db 488 LGTGNHGVVHPSLADSANKFEENTYCFGRVTETLLIRFGKTTIMEQVLKRVANILINL 547
QY 541 YGTAIVLSRASIRIRIGLRNHDHVEILLANTFCVEAYLQNLFSLSQLDKYPENLDBQIKK 600
Db 548 YGTAIVLSRASIRIRIGLRNHDHVEILLANTFCVEAYLQNLFSLSQLDKYPENLDBQIKK 607
QY 601 VSQOILEKRAYICAHPLDRTC 621
Db 608 VSQOILEKRAYICAHPLDRTC 628

RESULT 7
US-10-362-537-10
; Sequence 10, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Mouse
US-10-362-537-10

* Query Match 43.1%; Score 1360; DB 15; Length 655;
Best Local Similarity 48.2%; Pred. No. 2.7e-111;
Matches 287; Conservative 106; Mismatches 184; Indels 18; Gaps 9;

QY 35 PVRA-----FAKELFLGKIKKKEVFPPEV-SODELNEINQFLGPVEKFFTEEVDSRKIDQ 89
Db 66 PARAEKSKFAVGMFKGQLTIDQVPYPSVLSBEQAQFLKELGVPARFEEVNDPAKND 125
QY 90 EGIKPIDETLEKLSLGLFGLQVPEYGGFGFNTMYSRLGEIISM-DGSITVTLLAAHQAI 148
Db 126 LEKVEDDTLQGLKELGAFGLQVPSLGLGLSNTQYARLAEIVGMHDLGVSVTLGAHQSI 185
QY 149 GLKGITLAGTEOKAKYLPKLASGEHIAAFLCTEPASGSDAASIRSRATLSDEKHHYIN 208
Db 186 GFPGILLYGTAKQREKYLPRVAGQALAAFLCTEPSSGSDVASIRSAIPSPCGKYITLN 245
QY 209 GSKVWITNGLANIFVFAKTEVVD-SDGSVKDKITAFIVERDFGVNGKPDKLGIRG 267
Db 246 GSKIWLSNGGLADIFTVFAKTPKDAATGAVKEKITAFAVVERSGVTHGLPEKMGKIA 305
QY 268 SNTCEVHPENTKIPVENILGEVGDGFKVAMNLSGRFSMGVSVAGLLKRLIEMTAEYAC 327
Db 306 SNTSEVYFDGVKVPSENVLGEVGDGFKVAVNLLNNGFRGMAATLAGTMRSLIAKAVDHAT 365
QY 328 TRKQFNKRLSEFLIOEKALMAQKAYVMSMTYLTAGMLDQPGPPDCSIEAAWVKVFS 387
Db 366 NRTQFGDKIHNFQVIOEKALMAQKAYVMSMTYLTAGMLDQPGPPDCSIEAAWVKVFS 424
QY 388 EAAWQCVSEALQILGLGYTRDYPYERILDRTRILLIFEGTNEILRMVIALTGLQHAGRI 447
Db 425 EAAKWVADCEIQMGMGFWKPEGVVERVLRDIRIFRIFEGANDILRLFVALQCMKDGKE 484
QY 448 LTTTRIELKQ--AKVSTVMDTVGRRRLRSLGRYVDLGLTGNHGVVHPSLADSANKFEENT 505
```

```
Db 485 LTGLGNALKNPFGNVGLMGEAGKQURRTGIGSGLSLS---GIVHPELSRSGELAVQAL 541
QY 506 YCFGRVTETLLIRFGKTTIMEEQVLKRVANILINLYGMTAVLSRASIRIRIGLRNHDHEV 565
Db 542 DQPAIVVEAKLVKHKGIQVNEQFLQLRLADGALDYAMVVVLSRASRSLSEGYPYTAQHEK 601
QY 566 LIANTFCVRA---YLQNLFSLSQLDKYPENLDEQIKKVSQQILEKRAYICAHPL 617
Db 602 MLCDSWCIEAATRIRENMASSLOSSPOH--QELFRNFRSISKAMVENGGLVTGNPL 654

RESULT 8
US-10-362-537-9
; Sequence 9, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Rat
US-10-362-537-9

Query Match 43.0%; Score 1356.5; DB 15; Length 653;
Best Local Similarity 46.4%; Pred. No. 5.6e-111;
Matches 295; Conservative 108; Mismatches 192; Indels 41; Gaps 12;

QY 9 RTTAAARACRGLVSVSTANRRLLR-----TSPVRA-----FAKELFLGKIKKKEV 53
Db 32 RPTSAQR---LVASEATQAVLEKPELTSSDASTREKPARAEKSKFAVGMFKGQLTIDQV 87
QY 54 FPPPEVSQDELNE-----INQFLGPVEKFFTEEVDSRKIDQBGKI PDETLEKLSLGLFG 108
Db 88 FPPPSV-----LNEGQTQFLKELGVPARFEEVNDPAKNDLSLEKVEEDTLQGLKELGAFG 143
QY 109 LQVPEYGGFGFNTMYSRLGEIISM-DGSITVTLLAAHQAI GLKGIILACTEOKAKYLP 167
Db 144 LQVPSLGLGLSNTQYARLAEIVGMHDLGVSVTLGAHQSIGFKGILLVYTKAQEKYLP 203
QY 168 KLASGEHIAAFLCTEPASGSDAASIRSRATLSDEKHHYILNGSKVWITNGGLANIETVFA 227
Db 204 RVASGQALAAFLCTEPSSGSDVASIRSAVSPSPCGKYITLNGSKIWSNGGLADIFTVFA 263
QY 228 KTEVVD-SDGSVKDKITAFIVERDFGVNGKPDKLGIRGSGNTCEVHPENTKIPVENIL 286
Db 264 KTIKDAATGAVKEKITAFAVVERSGVTHGLPEKMGKIKASNTSEVYFDGVKVPANVL 323
QY 287 GEVGDGFKVAMNLSGRFSMGVSVAGLLKRLIEMTAEVACTRKQFNKRLSEFLIOEK 346
Db 324 GEVGDGFKVAVNLLNNGFRGMAATLAGTMRSLIAKAVDHATNTQFGDKIHNFVQSKL 383
QY 347 ALMAQKAYVMSMTYLTAGMLDQPGPPDCSIEAAWVKVFSSEAAWQCVSEALQILGLGY 406
Db 384 ARMAIILQVYTESMAYMLSANMDQ-GPKDFQIEAAISKIFGSEAAWVTDCEIQMGMGF 442
QY 407 TRDYPYERILDRTRILLIFEGTNEILRMVIALTGLQHAGRIILTRTHIELKQ--AKVSTVM 464
Db 443 MKEPGVVERVLRDIRIFRIFEGTNDILRLFVALQCMKDGKELTGLGNALKNPGLNGLLI 502
QY 465 DTVGRRLRSLGRYVDLGLTGNHGVVHPSLADSANKFEENTYCFGRVTETLLIRFGKTI 524
Db 503 GEASKQLRRRTGIGSGLSLS---GIVHPELSRSGELAVQALBOFATVTVREAKLMKKHKGIV 559
```

```

Qy 525 EEQLVLRKRVANILNLYGMTAVLSRASRSIRIGLRNHDHVEILLANTFCVEA---YLQNLF 581
Db 560 NEQFLQLRLADCAIDLAVMVVLSRASRSISEGPTAQHEKMLCDSWCIEAATRIENMA 619
Qy 582 SLSQLDKYAPENLDEQIKKVSQQILEKRAYICAHPL 617
Db 620 SLSQNPQ--QQELPRNFRSISKAMVENGGLVTSNPL 653

RESULT 9
US-10-362-537-11
; Sequence 11, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Bovine
US-10-362-537-11

Query Match 42.7%; Score 1345; DB 15; Length 655;
Best Local Similarity 47.3%; Pred. No. 5, 8e-110;
Matches 285; Conservative 110; Mismatches 194; Indels 14; Gaps 9;

Qy 23 STANRLRLTSPVPAPAKELFLGKIKKKEVFPPEV-SODELNEINQFLGPVEKPFTEE 81
Db 57 SEASTREKRANSVSKSPAVGTFKQLTTDQVFPYPSVLNDEQTFKLKELVGPVTRFEEV 116
Qy 82 VDSRKIDQCKIPDETLEKLSLGLFGLQVPEYGGVGFNTMYSLRGLHISM-DGSITV 140
Db 117 NDAKNDMLSERVETMQGKELGAGFGLQVPELGGVGLCNTQYARLVEIVGMDLGVGI 176
Qy 141 TLAHQAGLGLGKILAGTEQKAKYLPKLASGHEIAAFCLTEPASGSDAASIRSATLSE 200
Db 177 VLGAHQSIGFKGILLFTGKAQKYLPLKASGETIAAFCLTEPSSGSDAASIRSAVSP 236
Qy 201 DKHYILNGSKWITNGGLANIITVFAKTEVVD--SDGSVKDKITAFIVERDFGVTNGKP 259
Db 237 CGKYITLNGSKIWISNGGLADIITVFAKTPVTDATGAVKEKITAFVVERSGGVTHGPP 296
Qy 260 EDKLGIRGNTCEVHPENTKIPVENILGEVGDGFKVAMNLSNGRFSMGSVVAGLKRLLI 319
Db 297 EKGWIKASNTAEVYFDGVRPAENVLGEVGGFKVAMHLLNNGRFGMAALAGTWKGII 356
Qy 320 EMTAEYACTRKQFNKRLSEFGLIQEKFALMAQKAYMESMTYLTAGMLDQPGFPDCSIEA 379
Db 357 AKAVDHAANTQFGKIHNFGLIQELARWMLQYVVTESMAYMVSAAMDQ--GSTDFQIEA 415
Qy 380 AMVKVSSSEAQCSEALQILGGLGYTRDYPYVERILDRTRILLIFEGTNEILRMVIALT 439
Db 416 AISKIFGSEAAWKTDECIQIMGGMGFMKEPGVERVRLDRIRIFIEGNDILRLFVALQ 475
Qy 440 GLQHAGRLITRIHELKQ--AKVSTVMDTVGRRLRSLGRITVDLGTGNHGVVHPSLADS 497
Db 476 GCMWDKGKLSGLGNALKNPFGNAGLLGEAGKQLRRRAGLSGLSLS---GIVHQELSR 532
Qy 498 ANKFEENTYCFGRVETLLRFGKTIMEQVLKRVANILNLYGMTAVLSRASRSIRIG 557
Db 533 GELAVQALEQFATVWAKLHKHKKDIINEQFLQLRLADSAIDLAVMVVLSRASRSLS 592
Qy 558 LRNHDHVEILLANTFCVEA---YLQNLFSLSQLDKYAPENLDEQIKKVSQQILEKRAYICA 614
Db 593 HPTAQHEKMLCDSWCIEAARIENMTAL--QSDPQQOE--LFRNFKSISKALVERGGVTS 650

```

```

Qy 615 HPL 617
Db 651 NPL 653

```

```

RESULT 10
US-10-362-537-1
; Sequence 1, Application US/10362537
; Publication No. US20040086510A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: IRAP Binding Protein
; FILE REFERENCE: 2774 USOP
; CURRENT APPLICATION NUMBER: US/10/362,537
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2000-254263
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: JP 2000-276633
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 1
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Human
US-10-362-537-1

```

```

Query Match 41.5%; Score 1308; DB 15; Length 655;
Best Local Similarity 46.9%; Pred. No. 1, 1e-106;
Matches 276; Conservative 106; Mismatches 194; Indels 12; Gaps 8;

```

```

Qy 37 RAFAKELFLGKIKKKEVFPPEVFPPEV-SODELNE-INQFLGPVEKPFTEEVDSEKIDQEGKIPD 95
Db 71 KSFVGMFGKQLTTDQVFPYPSVLNDEQTFKLKELVGPVTRFEEVNDPAKNDALMEVVE 130
Qy 96 ETLEKLSLGLFGLQVPEYGGVGFNTMYSLRGLHISM-DGSITVTLAAHQAGLKGII 154
Db 131 TTWQGLKELGAGFGLQVPELGGVGLCNTQYARLVEIVGMDLGVGITLGAHQSIGFKGIL 190
Qy 155 LAGTEQKAKYLPKLASGHEIAAFCLTEPASGSDAASIRSATLSEDKHYILNGSKWIM 214
Db 191 LFTKAQKELPLKASGETVAAAFCLTEPSSGSDAASIRTSVPSGKYITLNGSKLWI 250
Qy 215 TNGGLANIITVFAKTEVVD--SDGSVKDKITAFIVERDFGVTNGKPEDKLGIRGNTCEV 273
Db 251 SNGGLADIITVFAKTPVTDATGAVKEKITAFVVERSGGITHGPEKKWGIKASNTAEV 310
Qy 274 HFENTKIPVENILGEVGDGFKVAMNLSNGRFSMGSVVAGLKRLLIEMTAEYACTRKQFN 333
Db 311 FPDGVRVPSENVLGEVSGFKVAMHLLNNGRFGMAALAGTWGIIAKAVDHAATNRTQFG 370
Qy 334 KRLSEFGLIQEKFALMAQKAYMESMTYLTAGMLDQPGFPDCSIEAMVKVSSSEAQC 393
Db 371 EKIHNFGLIQELARWMLQYVVTESMAYMVSAAMDQ--GATDFQIEAAISKIFGSEAAWKV 429
Qy 394 VSEALQILGGLGYTRDYPYVERILDRTRILLIFEGTNEILRMVIALTGLQHAGRLITRIH 453
Db 430 TDECQIMGGMGFMKEPGVERVRLDRIRIFIEGNDILRLFVALQCMGDKGKLSGLS 489
Qy 454 ELKQ--AKVSTVMDTVGRRLRSLGRITVDLGTGNHGVVHPSLADSANKFEENTYCFGR 511
Db 490 ALKNPFGNAGLLGEAGKQLRRRAGLSGLSLS---GLVHPELSRSGELAVRALQFATV 546
Qy 512 VETLLRFGKTIMEQVLKRVANILNLYGMTAVLSRASRSIRIGLRNHDHVEILLANTFF 571
Db 547 VBAKLIKHKHKKGIWNSQFLQLRLADCAIDLAVMVVLSRASRSLSSEGHPTAQHEKMLCDTW 606
Qy 572 CYE--AYLQNLFSLSQLDKYAPENLDEQIKKVSQQILEKRAYICAHPL 617
Db 607 CIEAARIRPEGMAALQSDPQQOE--LYRNFKSISKALVERGGVTSNPL 653

```

RESULT 11

Db	61	LADSANKFEENTYCFGRVTETLLRFGKTIMEEQVLKRVANILINDYGMTAVLSRSRS	120
Qy	554	IRIGLENDHDEVLANTFCVEAYLQNLFSLSQDKYAPENLDBQIKKVSQQILEKRAYIC	613
Db	121	IRIGLENDHDEVLANTFCVEAYLQNLFSLSQDKYAPENLDBQIKKVSQQILEKRAYIC	180
Qy	614	AHPLDRTC 621	
Db	181	AHPLDRTC 188	

Search completed: April 25, 2005, 17:39:17
 Job time : 136 secs

THIS PAGE BLANK (USPTO)